

## Appendix VI

Alignment of instant SEQ ID NO: 1 (nucleotides 770-1310) with SEQ ID NO: 1 of Sisk et al.

Score = 994 bits (538), Expect = 0.0  
 Identities = 540/541 (99%), Gaps = 0/541 (0%)  
 Strand=Plus/Plus

Query	770	GCCAAGAGTGAAGTACCGCCTATAGAGTCTATAGGCCACCCCTTGCGCTCTCTAT	829
Sbjct	713	GCCAAGAGTGAAGTACCGCCTATAGAGTCTATAGGCCACCCCTTGCGCTCTCTAT	772
Query	830	GCATGCTATACCTGTTTTTGCGCTTGCGGCTATACACCCCGCTTCCTCATGTTATAGGTG	889
Sbjct	773	GCATGCTATACCTGTTTTTGCGCTTGCGGCTATACACCCCGCTTCCTCATGTTATAGGTG	832
Query	890	ATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCACTATTGACCACTCCCTATTGG	949
Sbjct	833	ATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCACTATTGACCACTCCCTATTGG	892
Query	950	TGACGATACCTTCCATTACTAATCCATAACATGGCTCTTTGCCACCACTCTCTTTATTGG	1009
Sbjct	893	TGACGATACCTTCCATTACTAATCCATAACATGGCTCTTTGCCACCACTCTCTTTATTGG	952
Query	1010	CTATATGCCAATACACTGTCTCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGATGG	1069
Sbjct	953	CTATATGCCAATACACTGTCTCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGATGG	1012
Query	1070	GGTCTCATTTTATTTTACAAATTACATATACAACACCACCGTCCCAAGTGGCCGCAGT	1129
Sbjct	1013	GGTCTCATTTTATTTTACAAATTACATATACAACACCACCGTCCCAAGTGGCCGCAGT	1072
Query	1130	TTTTATTAAACATAACGTGGGATCTCCACGCGAATCTCGGGTACGTGTCTCCGGAACGGTG	1189
Sbjct	1073	TTTTATTAAACATAACGTGGGATCTCCACGCGAATCTCGGGTACGTGTCTCCGGAACGGTG	1132
Query	1190	GAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCCACCAAGACATAATAGC	1249
Sbjct	1133	GAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCCACCAAGACATAATAGC	1192
Query	1250	TGACAGACTAACAGACTGTTTCCTTTCCATGGGCTTTTCTGCAGTACCCGTCCTTCACAC	1309
Sbjct	1193	TGACAGACTAACAGACTGTTTCCTTTCCATGGGCTTTTCTGCAGTACCCGTCCTTCACAC	1252
Query	1310	G 1310	
Sbjct	1253	G 1253	